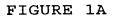
Inventor: GIJZEN SN 08/939,905/Sheet 1 of 15 Atty. Dkt.: 76-105



	ATGGGTTCCATGCGTCTATT	20
	M G S M R L L	
n	rx9+>	
ع .DTAGTGGCATTGTTGTGTGCATTGCTATGCATQ		80
V V A L L C A F A M H A		1
signal sequence	**	
GCTTACTCCTACGTTCTACAGAGAAACATGTCCAAA	######################################	140
GCTTACTCCTACGTTCTACAGAGAAACATGTCCAAA L T P T F Y R E T C P N		21
HIPIPIKEICIN		
prx12+>		
AATCTTCGATGCTTCTTTCACCGATCCCCGAATCGG		200 41
IFDASFTDPRIG	A S L M R L H F  active site	4.7
I	<	
TCATGATTGCTTTGTTCAAG GTTGTGATGGATCAG	STTTTGCTGAACAACACTGATACAAT	260
HDCFVQGCDGS	V L L N N T D T I	61
prx10 prx2+	>	
prx10	CAATAAGAGGATTGGACGTTGTCAA	320
ESEQDALPNINS		81
and the second s		380
TGACATCAAGACAGCGGTGGAAAATAGTTGTCCAGA		101
DIKTAVENSCPI		
II		
TGCTATTGCAGCTGAAATAGCTTCTGTTCTG GGA		440
A I A A E I A S V L G	G G P G W P V P L	121
AGGAAGAAGGGACAGCTTAACAGCAAACCGAACCC	TTGCAAATCAAAACCTTCCAGCACC	500
G R R D S L T A N R T	LANQNLPAP	141
TTTCTTCAACCTCACTCAACTTAAAGCTTCCTTTG	CTGTTCAAGGTCTCAACACCTTGA	560
	A V Q G I, N T L D	161
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		
III		(20
TTTAGTTACACTCTCAG GTGGTCATACGTTTGGA		620 1 <b>8</b> 1
heme-binding domain	RARCBIII	101
nemo binariig binarii		
CCGATTATACAACTTCAGCAACACTGGAAACCCTG		680
RLYNFSNTGNP	D P T L N T T Y L	201
AGAAGTATTGCGTGCAAGATGCCCCCAGAATGCAA	ACTGGGGATAACCTCACCAATTTGGA	740
E V L R A R C P Q N A		221
CCTGAGCACACCTGATCAATTTGACAACAGATAC	TACTCCAATCTTCTGCAGCTCAATGG	800
L S T P D Q F D N R Y		241

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# FIGURE 1B

CTTA	СТТ	CAG.	AGT	GAC	CAA	GAA	СТТ	TTC	TCC	ACT	CCT	GGT	GCT	GAT	'ACC	TTA	CCC	TTA	GT	860
	L	Q	S	D	Q	E	L	F	S	T	P	G	A	D	Т	I	P	I	V	261
							_			nrx	6 -									
CAAT	AGC	ттс	AGC	AGT	AAC	CAG									GTT	TCA	ATG	ATA	AA	920
N	S	F	s	S	N	Q	N	Т	F	F	S	И	F	R	V	S	М	I	K	281
AATG	יממת	ייעממי	יידי בי	'GGA	GTG	CTG	ACT	'GGG	GAT	'GAA	GGF	AGAA	LTA	'CGC	TTC	CAF	ATGT	raa'	TT	980
M	G	N	Т	G	V	L	Т	G	D	E	G	E	Ι	R	L	Q	C	N	F	301
••	J	-	•	_																
TGTO	חתתי	יכפז	C A C	ייייכר	<u>፣</u> ጥጥባ	rggz	ጥጥድ	\GCT	יאקי	rgre	GCC	TCC	CAA	AGAT	rgc:	(AA)	ACAF	)AA	3CT	1040
V	N	G. G	JADI D	S	न	G	Τ.	 A	S	V	A	S	К	D	А	K	Q	K	L	321
V	14	J		٥	•	•	_		_											
																~ ~ ~				3300
TGT	rgc:	rcai	ATC:	IAA1	ATA	AACC	'AA'	raa:	rta.	ATG(	3GG2	ATG'	rgc.	ATG	CTA	GCT.	AGC	A.I.G.	raa	1100 326
V	A	Q	S	K	*															320
AGG	CAA	ATTA	AGG'	TTG	TAAT	ACC.	гст	rtg	CTA	GCT.	ATA	TTG	AAA	AAT	ACC.	AAA	GGA	GTA	GTG	1160
																		~		1000
TGC.	ATG'	TCA	TTA	CGA'	TTT	TGC	CAT	GTA	CCT	CTT	GGA	ATA	ATT	TGT	TAAT	AAT	TAT'	TTG.	AA'I'	1220
CTC	ագու	カカご	ፈሞ <b>ኦ</b>	CTT	ידים מ	' מ מיד	דכ (	A) n												
CIC	T T T	יטריט.	חיני	C 1 1.			_ ~ (	,												



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#### FIGURE 2A

50 60 1.0 20 3.0 40 1 GCATCATATCATAAACAATACGTACGTGATATTATCTAGTGTCTCTCAGTTTACTTTATG 61 AGAAATTATTTTTTTTTAAAAAAAGTTAATTAATAAAAACATTTGCGATACCGTGAGTTA 121 CAAGAAATCCGCCGAATTCATCTCTATAAATAAAAGGATCTATATGAGAGGTAAAATCAT 181 ATTAACTCAAAATGGGTTCCATGCGTCTATTAGTAGTGGCATTGTTGTGTGCATTTGCTA 241 TGCATGCAGGTTTTTCAGTCTCTTATGCTCAGCTTACTCCTACGTTCTACAGAGAAACAT 301 GTCCAAATCTGTTCCCTATTGTGTTTGGAGTAATCTTCGATGCTTCTTTCACCGATCCCC 421 TTTTTTTTCCTTCCAAAATGCCCTGCATATTTAACAAGATTGCTTTGTTCACCTAGAAAA 541 GATCAAGAAAATAGCTAGAAAGAAAGCAACGTTTTTTTAAAAAGGTATTTAGTGTGAGAAA 501 AATATTAAAACTGAAGAGAAAGAAATTAAATAAGCTTTTCTTGAATGATATTTACATGTC 661 TTATTAACTTAAAGTCACCTTTTTTCTTTAAGTTGTGCTTGAAGAAAAAAAGATGTCTTTC 731 TTTACCATATTAATTACTATATTTCATGATGACAACAGACAAGTATTCTAAAGAGGT 841 ATCGGTAGATGATTAATTTTTTTATAAAAAAATCTTTTGCGTGTATAGATATTCTTTAT 901 AATTGGTGCAGAAACTTGTAATGCTAATTGCAATTAATCTTACATTGATTAACTAATAGC 961 TATAATCAATATTTAGGTTAGGTATAGGAGACAAATCAAGTGATCTGAACAAATTAAGTT 1021 GTTATATTTGCATTGTGACAGGGTTGTGATGGATCAGTTTTTGCTGAACAACACTGATACA 1981 ATAGAAAGCGAGCAAGATGCACTTCCAAATATCAACTCAATAAGAGGATTGGACGTTGTC 1141 AATGACATCAAGACAGCGGTGGAAAATAGTTGTCCAGACACAGTTTCTTGTGCTGATATT 1261 AACCATTAAAAAGTTGCATGATTGGATTCAAAATTCTATGGTATTGGGGTTCTGATATAA 1501 GGATGGAATCAGTCAAAACATTTAATTCAAAATACTCTTAATTGTGATTAGTAATCATGT 1621 GCAAGCCGGTTGGTATAGATATCACTGGCCTGTAGAATATGTGGTTTTTCACGTTTAAAT 1741 TATTGACTGTGAAACATGTTTCCACACACAGGCTTAGAAACTCCTCGCAACTAACATCTC 1801 CAAAATTTGACTATTTATTATGAAGATAATTCATCTATGATGTTCAACTCTATTATATA 1861 TATGTATCATCGCAGTATTAAGAATTATAATAGTCAAATATAGAAGTATATCGGGTAAAT 1921 GTAGTTGCATGTGCACCTGTTTCGTGTAAAATGCTTATTCTATATAGCTTTTTTTATTG 1981 GAAAATAACGATGAACTAAAAACGAAAGGGTATCATATAGTTTGACTTTTATGTTAGAGA 2041 GAGACATCTTAATTTGGTCATATGTTAAATAATTAATTACAATGCATACACAAATATTTA 2101 TGCCATATCTAAAAAATGATAAAATATCATAGGTATACTCAACTATATGATATCCCCATA 2221 ATCCACTTAAAGTGGTTCAACATATTTATGTAATAATTTACAGGGAGGAGGTCCAGGATG



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# FIGURE 2B

2281	$\tt GCCAGTTCCATTAGGAAGAAGGGACCGTTAACAGCAAACCGAACCCTTGCAAATCAAAA$
2341	$\tt CCTTCCAGCACCTTTCTTCAACCTCACTCAACTTAAAGCTTCCTTTGCTGTTCAAGGTCT$
2401	${\tt CAACACCCTTGATTTAGTTACACTCTCAGGTATACATAATCAATTTTTTTT$
2461	GCTAGCAATAAAAAGTCTCTGATACAGACATATTTAGATAAATTAATT
2521	${\tt TTTATAAAAATTATCAATTTATGTACTTAAAAATTATGGATTGAAGCTCTTTTCATCC}$
2581	${\tt AACTTTTACTAAAGTTAAGGTGCATATAATATAAAATAAACTATCTCTTGTTTCTTATAA}$
2641	${\tt AAAGATTGAAGATAAGTTAAAGTCTACTTATAAATCATTAATATATGTATAGGTGGTCAT}$
2701	${\tt ACGTTTGGAAGAGCTCGGTGCAGTACATTCATAAACCGATTATACAACTTCAGCAACACT}$
2761	GGAAACCCTGATCCAACTCTGAACACAACATACTTAGAAGTATTGCGTGCAAGATGCCCC
2821	${\tt CAGAATGCAACTGGGGATAACCTCACCAATTTGGACCTGAGCACACCTGATCAATTTGAC}$
2881	AACAGATACTACTCCAATCTTCTGCAGCTCAATGGCTTACTTCAGAGTGACCAAGAACTT
2941	$\tt TTCTCCACTCCTGGTGCTGATACCATTCCCATTGTCAATAGCTTCAGCAGTAACCAGAAT$
3001	${\tt ACTTTCTTTTCCAACTTTAGAGTTTCAATGATAAAAATGGGTAATATTGGAGTGCTGACT}$
3061	$\tt GGGGATGAAGGAGAAATTCGCTTGCAATGTAATTTTGTGAATGGAGACTCGTTTGGATTA$
3121	${\tt GCTAGTGTGGCGTCCAAAGATGCTAAACAAAAGCTTGTTGCTCAATCTAAATAAA$
3181	${\tt AATTAATGGGGATGTGCATGCTAGCTAGCATGTAAAGGCAAATTAGGTTGTAAACCTCTT}$
3241	$\tt TGCTAGCTATATTGAAATAAACCAAAGGAGTAGTGTGCATGTCAATTCGATTTTGCCATG$
3301	TACCTCTTGGAATATTATGTAATAATTATTTGAATCTCTTTAAGGTACTTAATTAA

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### FIGURE 3A-(1)

L78163	ATGGGTTCCATGCGT-CTATTAGTAGTGGCATTGTTG	36
U41657		0
X90693	${\tt GGCAAA-CAATGAACTCCCTTCGTGCTGTAGCAATAG-CTTTGTGC}$	44
X90694	GCTCTTCAAAACAATGAACTCCTTAGCAACTT-CTATGTGG	40
L36156	TTAGCAACTT-CTATGTGG	53
X90692	AATGCTTGGTCTAAGTGCAACAGCTTTTTGCTGTATGG	38
L78163	TGTGCATTT-GCTATGCATGCAGGTTTTTCAGTCTCTTATGC	77
U41657		0
X90693	${\tt TGTATTGTGGTTGTGCTTGGAGGGTTACCCTTCTCTAAATGC}$	88
X90694	TGTGTTGTGCTTTAGTTGTGCTTGGAGGACTACCCTTTTCCTCAGATGC	90
L36156	TGTGTTGTGCTTTAGTTGTGCTTGGAGGACTACCCTTTTCCTCAGATGC	72
X90692	TGT-TTGTGCTAATTGGAGGAGTACCCTTTTCAAATGC	75
170162	TCAGCTTACTCCTACGTTCTACAGAGAAACATGTCCAAATCTGTTCCCTA	127
L78163	TCAGCTTACTCCTACGTTCTACAGAGAAACATGTCCAMMTCTGTTCCGAM	0
U41657	GCAACTTGATCCATCCTTTTACAGGAACACTTGTCCAAATGTTAGTTCCA	138
X90693	ACAACTTAGTCCCACTTTTTACAGCAAAACGTGTCCAACTGTTAGTTCCA	140
X90694	ACAACTTAGTCCCACTTTTTACAGCAAAACGTGTCCAACTGTTAGTTCCA ACAACTTAGTCCCACTTTTTACAGCAAAACGTGTCCAACTGTTAGTTCCA	122
L36156	ACAACTTAGTCCCACTTTTTACAGCAAAACGTGTCCAACTGTTAGTTCCA ACAACTAGATCCTTCATTTTACAACAGTACATGTTCTAATCTTGATTCAA	125
X90692	ACAACTAGATCCTTCATTTTACAACAGTACATGTTCTAATCTTGATTCAA	123
L78163	TTGTGTTTGGAGTAATCTTCGATGCTTCTTTCACCGATCCCCGAATCGGG	177
U41657		0
X90693	TTGTTCGTGAAGTCATAAGGAGTGTTTCTAAGAAAGATCCTCGTATGCTT	188
X90694	TTGTTAGCAATGTCTTAACAAACGTTTCTAAGACAGATCCTCGCATGCTT	190
L36156	TTGTTAGCAATGTCTTAACAAACGTTTCTAAGACAGATCCTCGCATGCTT	172
X90692	TCGTACGTGGTGTGCTCACAAATGTTTCACAATCTGATCCCAGAATGCTT	175
	GCCAGTCTCATGAGGCTTCATTTTCATGATTGCTTTGTTCAAGGTTGTGA	227
L78163		227
U41657	TTTCATGATTGCTTCTCAAGGTTGTGA	238
X90693	GCTAGTCTTGTCAGGCTTCACTTTCATGACTGTTTTGTTCAAGGTTGTGA	240
X90694	GCTAGTCTCGTCAGGCTTCACTTTCATGACTGTTTTGTTCTGGGATGTGA	222
L36156	GCTAGTCTCGTCAGGCTTCACTTTCATGACTGTTTTGTTCTGGGATGTGA	225
X90692	GGTAGTCTCATCAGGCTACATTTTCATGACTGTTTTGTTCAAGGTTGCGA	245
	****** ** ****** ** **	
L78163	TGGATCAGTTTTGCTGAACAACACTGATACAATAGAAAGCGAGCAAGATG	277
U41657	TGGATCAGTTTTACTGAACAACACTGATACAATAGAAAGCGAGCAAGATG	79
X90693	TGCATCAGTTTTACTAAACAAAACTGATACCGTTGTGAGTGA	288
X90694	TGCCTCAGTTTTGCTGAACAATACTGCTACAATCGTAAGCGAACAACAAG	290
L36156	TGCCTCAGTTTTGCTGAACAATACTGCTACAATCGTAAGCGAACAACAAG	272
X90692	TGCCTCGATTTTGCTGAACGATACGGCTACAATAGTGAGCGAGC	275
	** ** ** *** ** * * * * * * * * * * * *	
L78163	CACTTCCAAATATCAACTCAATAAGAGGATTGGACGTTGTCAATGACATC	327
U41657	CACTTCCAAATATCAACTCAATAAGAGGATTGGACGTTGTCAATGACATC	129
X90693	CTTTTCCAAACAGAAACTCATTAAGAGGTTTGGATGTTGTGAATCAAATC	338
X90694	CTTTTCCAAATAACAACTCTCTAAGAGGTTTGGATGTTGTGAATCAGATC	340
L36156	CTTTTCCAAATAACAACTCTCTAAGGGGTTTGGATGTTGTGAATCAGATC	322
X90692	CACCACCAAATAACAACTCCATAAGAGGTTTGGATGATAAACCAGATC	325
	* **** * **** *** **** ** * * * * * * *	

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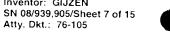
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# FIGURE 3A-(2)

L78163	AAGACAGCGGTGGAAAATAGTTGTCCAGACACAGTTTCTTGTGCTGATAT	3//
U41657	AAGACAGCGGTGGAAAATAGTTGTCCAGACACAGTTTCTTGTGCTGATAT	179
X90693	AAAACAGCTGTGGAAAAGGCTTGTCCTAACACAGTTTCTTGTGCTGATAT	388
X90694	AAACTGGCTGTAGAAGTGCCTTGTCCTAACACAGTTTCTTGTGCTGATAT	390
L36156	AAAACTGCTGTAGAAAGTGCTTGTCCTAACACAGTTTCTTGTGCTGATAT	372
	AAAACAGCGGTGGAAAATGCTTGTCCTAACACAGTTTCTTGTGCTGATAT	375
X90692	**	
L78163	TCTTGCTATTGCAGCTGAAATAGCTTCTGTT-CTGGGAGGAGGTCCAGGA	426
U41657	TCTTGCTATTGCAGCTGAAATAGCTTCTGTTGCTGGGAGGAGGTC-AGGA	228
X90693	TCTTGCTCTTTCTGCTGAATTATCATCTACA-CTGGCAGATGGTCCTGAC	437
X90694	TCTTGCACTTGCTCCAAGCATCCTCTGTT-CTGGCACAAGGTCCTAGT	439
L36156	TCTTGCACTTGCTCAAGCATCCTCTGTT-CTGGCACAAGGTCCTAGT	418
X90692	TCTTGCTCTTTCTGCTGAAATATCATCTGAT-CTGGCAAATGGTCCTACT	424
X70072	***** ** * * * * * * * * * * * * * * * *	
L78163	TGGCCAGTTCCATTAGGAAGAAGGGACAGCTTAACAGCAAACCGAACCCT	476
U41657	TGGCCAGTTCCATTAGGAAGAAGGGACAGCTTAACAGCAAACCGAACCCT	278
X90693	TGGAAGGTTCCTTTAGGAAGAAGAGATGGTTTAACGGCAAACCAGTTACT	487
X90694	TGGACGGTTCCTTTAGGAAGAAGGGATGGTTTAACCGCAAACCGAACACT	489
L36156	TGGACGGTTCCTTTAGGAAGAAGGGATGGTTTAACCGCAAACCGAACACT	468
	TGGCAAGTTCCATTAGGAAGAAGGGATAGTTTGACAGCAAATAATTCCCT	474
X90692	**	
L78163	TGCAAATCAAAACCTTCCAGCACCTTTCTTCAACCTCA-CTCAACTTA	523
U41657	TGCAAATCAAAACCTTCCAGCACCTTTCTTCAACCTCA-CTCAACTTA	325
X90693	TGCTAATCAAAATCTTCCAGCTCCTTTCAATACTACTGATCAACTTA	534
X90694	TGCAAATCAAAATCTTCCGGCTCCATTCAATTCCTTGGATCAACTTA	536
L36156	TGCAAATCAAAATCTTCCGGCTCCATTCAATTCCTTGGATCACCTTA	515
X90692	TGCAGCTCAAAATCTTCCTGCCCCCACTTTCAACCTTA-CTCGACTAA	521
130032	***. ***** **** ** ** *** * **. **.	
L78163	AAGCTTCCTTTG-CTGTTCAAGGTCTCAACACCCTTGATTTAGTTACACT	572
U41657	AAGCTTCCTTTG-CTGTTCAAGGTCTCAACACCCTTGATTTAGTTACACT	374
X90693	AAGCTGCATTTG-CTGCTCAAGGTCTCGATACTACTGATCTGGTTGCACT	583
X90694	AAGCTGCATTT-ACTGCTCAAGGCCTCAATACTACTGATCTAGTTGCACT	585
L36156	AA-CTGCATTTGACTGCTCAAGGCCTCATTACTCCTGTTCTAGTTGCCCT	564
X90692	AATCTAACTTTGA-TAATCAAAACCTCAGTACTACTGATCTAGTTGCACT	570
A90092	** **. *** *. ****. ** **. * * * * * *	
L78163	CTCAGGTGGTCATACGTTTGGAAGAGCTCGGTGCAGTACATTCATAAACC	622
U41657	CTCAGGTGGTCATACGTCTGGAAGAGCTCGGTGCAGTACATTCATAAACC	424
X90693	CTCCGGTGCTCATACATTTGGAAGAGCTCATTGCTCTTTATTTGTTAGCC	633
X90694	CTCGGGTGCTCATACATTTGGAAGAGCTCATTGCGCACAATTTGTTAGTC	635
L36156	CTCGGGTGCTCATACATTTGGAAGAGCTCATTGCGCACAATTTGTTAGTC	614
X90692	CTCAGGTGGCCATACAATTGGAAGAGGTCAATGCAGATTTTTCGTTGATC	620
A90692	*** ***	
L78163	GATTATACAACTTCAGCAACACTGGAAACCCTGATCCAACTCTGAACACA	672
U41657	GATTATACAACTTCAGCAACACTGGACTGATCCA-CT-TGGACACA	468
X90693	GATTGTACAACTTCAGCGGTACGGGAAGTCCCGATCCAACTCTTAACACA	683
X90694	GATTGTACAACTTCAGCAGTACTGGAAGTCCCGATCCAACTCTTAACACA	685
L36156	GATTGTACAACTTCAGCAGTACTGGAAGTCCCGATCCAACTCTTAACACA	664
X90692	GATTATACAATTTCAGCAACACTGGAAACCCCGATTCAACTCTTAACACG	670
	*** **** **** ** ** * * * * * * * * * *	

TRADEMENT

Inventor: GIJZEN



# FIGURE 3A-(3)

L78163	ACATACTTAGAAGTATTGCGTGCAAGATGCCCCCAGAATGCAACTGGGGA	722
U41657	ACATACTTAGAAGTATTGCGTGCAAGATGCCCCCAGAATGCAACTGGGGA	518
X90693	ACTTACTTACAACAATTGCGCACAATATGTCCCAATGGTGGACCTGGCAC	733
X90694	ACTTACTTACAACAACTGCGCACAATATGTCCCAATGGTGGACCTGGCAC	735
L36156	ACTTACTTACAACAACTGCGCACAATATGTCCCAATGGTGGACCTGGCAC	714
X90692	ACCTATTTACAAACATTGCAAGCAATATGTCCCAATGGTGGACCTGGTAC	720
	** ** *** * * ****** *** * ** * **** .	
L78163	TAACCTCACCAATTTGGACCTGAGCACCCTGATCAATTTGACAACAGAT	772
U41657	TAACCTCACCAATTTGGACCTGAGCACACCTGATCAATTTGACAACAGAT	568
X90693	GAACCTTACCAATTTCGATCCAACGACTCCTGATAAATTTGACAAGAACT	783
X90694	AAACCTTACCAATTTCGATCCAACGACTCCTGATAAATTTGACAAGAACT	785
L36156	AAACCTTACCAATTTCGATCCAACGACTCCTGATAAATTTGACAAGAACT	764
X90692	AAACCTAACCGATTTGGACCCAACCACACCAGATACATTTGACTCCAACT	770
	***** *** *** * * * * * * * * * * * * *	
	ACTACTCCAATCTTCTGCAGCTCAATGGCTTACTTCAGAGTGACCAAGAA	822
L78163		618
U41657	ACTACTCCAATCTTCTGCAGCTCAATGGCTTACTTCAGAGTGACCAAGAA	833
X90693	ATTACTCTAATCTTCAAGTGAAAAAAGGTTTGCTTCAAAGTGATCAAGAG	
X90694	ATTACTCCAATCTTCAAGTGAAAAAGGGTTTGCTCCAAAGTGATCAAGAG	835
L36156	ATTACTCCAATCTTCAAGTGAAAAAGGGTTTGCTCCAAAGTGATCAAGAG	814
X90692	ACTACTCCAATCTCCAAGTTGGAAAGGGCTTGTTTCAGAGTGACCAAGAG	820
	* **** **** * **.** **. * **.*** ****.	
L78163	CTTTTCTCCACTCCTGGTGCTGATACCATTCCCATTGTCAATAGCTTCAG	872
U41657	CGTTTCTCCACTCCTGGTGCTGATACCATTCC-ATTGTCAATAGCTTCAG	667
X90693	TTGTTCTCAACATCTGGTTCAGATACCATTAGCATTGTCAACAAATTCGC	883
X90693 X90694	TTGTTCTCAACTTCTGGTGCAGATACCATTAGCATTGTCAACAAATTCAG	885
L36156	TTGTTCTCAACTTCTGGTGCAGATACCATTAGCATTGTCGACAAATTCAG	864
X90692	CTTTTTCCAGAAATGGTTCTGACACTATTTCTATTGTCAATAGTTTCGC	870
X90092	** ** * . ****.** ** *** ****.* *. ***.	
L78163	CAGTAACCAGAATACTTTCTTTTCCAACTTTAGAGTTTCAATGATAAAAA	922
U41657	${\tt CGAACCAGAATACTTTCTTTTCCAACTTTAGAGTTTCAATGATAAAAA}$	715
X90693	AACCGATCAAAAAGCTTTTTTTGAGAGCTTTAGGGCTGCTATGATCAAAA	933
X90694	CACCGATCAAAATGCTTTCTTTGAGAGCTTTAAGGCTGCAATGATTAAAA	935
L36156	CACCGATCAAAATGCTTTCTTTGAGAGCTTTAAGGCTGCAATGATTAAAA	914
X90692	CAATAATCAAACTCTCTTCTTTGAAAATTTTGTAGCCTCAATGATAAAAA	920
	* ** * . ** *** * . * * * . * . * ***	
		972
L78163	TGGGTAATATTGGAGTGCTGACTGGGGATGAAGGAGAAATTCGCTTGCAA	765
U41657	TGGGTAATATTGGAGTGCTGACTGGGGATGAAGGAGAAATTCGCTTGCAA	983
X90693	TGGGAAATATTGGTGTTTAACCGGGAACCAAGGAGAGATTAGAAAACAA	985
X90694	TGGGCAATATTGGTGTGCTAACAGGGACAAAAGGAGAGATTAGAAAACAA	
L36156	TGGGCAATATTGGTGTGCTAACAGGGACAAAAGGAGAGATTAGAAAACAA	964
X90692	TGGGTAATATTGGAGTTTTAACTGGATCTCAAGGTGAAATTAGAACACAG	970
	**** ******** ** * * * * * * * * * * * *	
L78163	TGTAATTTTGTGAATGGAGACTCGTTTGGATTAGC	1007
U41657	TGTAATTTTGTGAATGGAGACTCGTTTGGATTAGC	800
X90693	TGCAACTTTGTTAATTCAAAATCAGCAGAACTTGGTCTTAT	1024
X90694	TGCAACTTTGTGAACTTTGTGAACTCAAATTCTGCAGAACTAGATTTAGC	1035
L36156	TGCAACTTTGTGAACTCAAATTCTGCAGAACTAGATTTAGC	1005
X90692	TGTAATGCTGTGAATGGGAATTCTTCTGGATTGGC	1005
	**	



# FIGURE 3A-(4)

T 70162	TAGTGTGGCGTCCAAAGATGCTAAACAAAAGCTTGTTGCTCAATCTAAAT	1057
L78163	TAGTGTGGCGTCCAAAGATGCTAAACAAAAGCTTGTTGCTCAATCTAAAT	850
U41657	CAATGTTGCCTCAGCAGATTCATCTG-AGGAGGGTATGGTTAG	1066
X90693	CACCATAGCATCCATAGTAGAATCATTAG-AGGATGGTATTGCTAGTG	1082
X90694	CACCATAGCATCCATAGTAG - AATCATTAG - AGGATGGAATTGCTAGTG	1052
L36156	TACTGTAGTCACCAAAGAATCATCAG-AAGATGGAATGGCTAGCT	1049
X90692	* * * * * * * * * * * * * * * * * * *	
T 00163	AAACCAATAATTAATGGGGATGTGCATGCTAGCTAGCATGTAAAGGCAAA	1107
L78163	AAACCAATAATTAATGGGGATGTCGATGCTAGCTACGATGTAAAGGCAAA	900
U41657	AAACCAATAATTAATGGGGTTGTGGTGTAAA-TG-TAG	1082
X90693	TAATATAAATAAATTAGCGTAAATGCACTTATTGAA-ATCTTG	1124
X90694	TAATATAAATAAATTAGCGAAAATGCACTTATTGAA-ATCTTG	1094
L36156	CATTCTAAAT - ATAAG CTTGGAAAATATTGAAGAGGTTCTAT	1090
X90692	CATICIAAA*	
		1157
L78163	TTAGGTTGTAAACCTCTTTGCTAGCTATATTGAAATAAACCAAAGGAGTA	949
U41657	TTAGGTTG-AAACCTCTTTGCTAGCTATATTGAAATAAACCAAAGGAGTA	1119
X90693	TGATTGGAAGCAACTAATAAATTAAGAAGCTATAACT	1119
X90694	TGACTAGATGCCACTAATAAATAAGTTATAACT	
L36156	TGACTAGATCCCACTAATAAATAAGTTATAACT	1127
X90692	AATTTTGTGCATACATATATGGTATGTG	1118
	, ***	
	GTGTGCATGTCAATTCGATTTTGC-CATGTACCTCTTGGAATAT	1200
L78163	GTGTCGATGTCAATTCGATTTTGC-CATGTACCTCTTGGAATATTATGTA	998
U41657	ATGCACATT-CATGGTATGTGAGATAGTTATTAGATGCTTTGTGAGCA	1168
X90693	AGGCACATT CATGGTM STOP AGGCACATTCATGCCT - GTATATGAG	1200
X90694	AGGCACATTTCATGTCACTTGAAATCCTATGCCTTGTATATTAGAGGACG	1177
L36156	CATGTGGTGTATTATGTTTTTGTTATGTTCTTCAAGTTGATCA	1161
X90692	****	
L78163	1200	
U41657	ATAATTATTTGAATCTCAAAAAAAAAAAAAAA 1031	
X90693	AAAATCTTTTGGATTTCATTTGAAGTGTTTCT 1200	
X90694	1200	
L36156	TGT-TCTTCTTGGTATTATACTAT 1200	
X90692	GGGA-CTGTAGAAGCTCCCTAATAATATTTGTGTCAAAGT 1200	
1.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		

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#### FIGURE 3B

1.78163	MGSMRLLVVALLCAFAMHAGFSVSYAQLTPTFYFETCPNLFPIVFGV	4.7 0
U41657 X40693	MNSLRAVAIALCCIVVVLGGLPFSSNAQLDPSFYENTCPNVSSIVREV	43
X30694	MNSLATSMWCVVLLVVLGGLPFS3DAQLSPTFYSKTCPTV3SIVSNV	4.7
L36156	MWCVVLLVVLGGLPFSSDAQLSPTFYSKTCPTVSSIVSNV	40
X90693	MLGLSATAFCCMVFVLIGGVPFS-NAQLDPSFYNSTCSNLDSIVRGV	$4 m \acute{n}$
L/8163	IFDASFTDPPIGASLMRLHEHDCFVQGCDGSVLLNNTDTIESEQDALPNI	37
U41657	FHDCFVQGCDGSVLLNNTDTIESEQDALPNI	31
х90693	IRSVSKKDPRMLASLVRLHFHDCFVQGCDASVLLNKTDTVVSEQDAFPNR	98 97
X90694	I.TNVSKTDPRMLASLVRLHFHDCFVLGCDASVLLNNTATIVSEQQAFPNN LTNVSKTDPRMLASLVRLHFHDCFVLGCDASVLLHNTATIVSEQQAFPNN	90
L36156 X90692	LTHVSQSDPRMLGSLIRLHFHDCFVQGCDASILLHDTATIVSEQSAPPHN	96
1,00002	***** *** * * * * * * * * * * * * * * *	
1.78163	NS 1RGLDVVNDIKTAVENSCPDTVSCADILAIAAEIASVLGGGPGWPVPL	147 81
041657	NSIRGLDVVNDIKTAVENSCEDTVSCADILAIAAEIASVAGRRSGWPVPL NSLRGLDVVNQIKTAVEKACENTVSCADILALSAELSSTLADGEDWKVPL	148
%90693 %90694	NSLRGLDVVNQIKTAVEARCENTVSCADITALBARDISSITEADGE BIKVET NSLRGLDVVNQIKLAVEVPCPNTVSCADITALAAQASSVLAQGPSWTVPL	147
L36156	MSLRGLDVVNQIKTAVESACPNTVSCADILALA-QASSVLAQGPSWTVPL	139
X90692	NSTRGLDVINOIKTAVENACPNTVSCADILALSAEISSDLANGPTWQVPL	146
1.50052	* **** * ** *** ** ****** * * * * * * *	
1.78163	GRRDSLTANRTLANQNI.PAPFFNLTQLKASFAVQGLNTLDLVTLSGGHTF	197
U41657	GRRDSLTANRTLANONLPAPFFNLTOLKASFAVOGLNTLDLVTLSGGHTS	131
X90693	GRRDGLTANOLLANONLPAPFNTTDQLKAAFAAQGLDTTDLVALSGAHTF	198
X90694	GRRDGLTANRTLANONLPAPFNSLDQLKAAFTAQGLNTTDLVALSGAHTF	197
L36156	GRRDGLTANRTLANONLPAPFNSLDHLKLHLTAQGLITPVLVALSGAHTF GRRDSLTANNSLAAQHLPAPTFNLTKLKSNFDNQNLSTTDLVALSGGHTI	189 196
X90692	SKEDSLIANNSDAAQHDEAFIENLIKDRSNEDNQNDSIIDDIADSGAII	150
L78163	GEARCSTFINELYNFSNTGNPDPTLNTTYLEVLFAPCPQNATGDNLTNLD	247
U41657	GRARCSTFINRLYNFSNTGLIHLDTTYLEVLPARCPQNATGDNLTNLD	179 248
M90693	GRAHOSLFVSRLYNFSGTGSPDPTLNTTYLQQLPTICPNGGPGTNLTNFD GRAHCAQFVSRLYNFSSTGSPDPTLNTTYLQQLRTICPNGGPGTNLTNFD	247
∷90694 L36156	GEAHCAQEVSRLYNESSIGSEDETLITTYLQQLETICPNGGEGTNLTNED	<u>- 39</u>
X90692	GRGOCRFFVDRLYNFSNTGNFDSTLNTTYLQTLQAICPNGGPGTNLTDLD	246
110001	** * * ***** ** * * * * * * * * * * * *	
L78163	LSTPDQFDNRYYSNLLQLNGLLQSDQELFSTPGADTIPIVNSFSSNQNTF	297
U41657	LSTPDQFDNRYYSNLLQLNGLLQSI/QERFSTPGADTIPLSIA-SANQNTF	228 298
X90693	PTTPDKFDKNYYSNLQVKKGLLQSDQELFSTSGSDTISIVNKFATDQKAF PTTPDKFDKNYYSNLQVKKGLLQSDQELFSTSGADTISIVNKFSTDQNAF	297
X90694	PTTPDKFDKNYYSNLQVKKGLLQSDQELFSTSGADTISIVDKFSTDQNAF	239
L36156 X90692	PTTPDTFDSNYYSNLQVGKGLFQSLQELFSRNGSDTISIVNSFANNQTLF	296
170163	FSNFRVSMIKMGNIGVLTGDEGEIRLQCNFVNGDSFGLASVAS-K	341
1.78163 U41657	FSNFRVSMIKMGNIGVLTGDEGEIFLQCNFVNGDSFGLASVAS-K	272
X90693	FESFRAAMIKMGNIGVLTGNOGEIREOONEVNSKSAELGLINVAS-A	344
2.90694	FESFKAAMIKMGNIGVLTGTKGEIPKQCNFVNFVNSNSAELDLATIASIV	347
L36156	FESFKAAMIKMGNIGVLTGTHGEIRFQCNFVNSNSAELDLATIASIV	336 340
X90692	FENFVASMIKMGNIGVLTGSQGEIKTQCNAVNGNSSGLATVVT-K ************* *** *** ***	240
L78163	DAKQKLVAQSK 352	
041657	DAKQKLVAQSK 283	
X90693	DSSEEGMVSJM 355 ESLEDGIASVI 358	
K90694 L36156	ESLEDGIASVI 358 ESLEDGIASVI 347	
X90692	ESSEDGMASSF 351	

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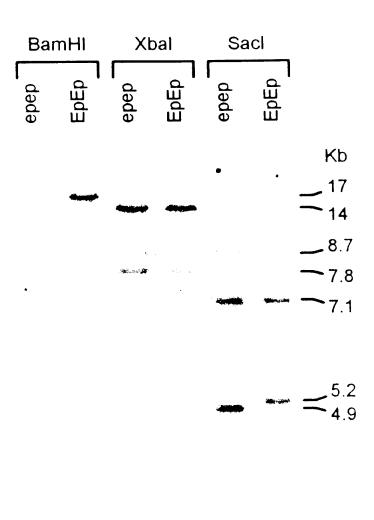


FIGURE 4

-3.4



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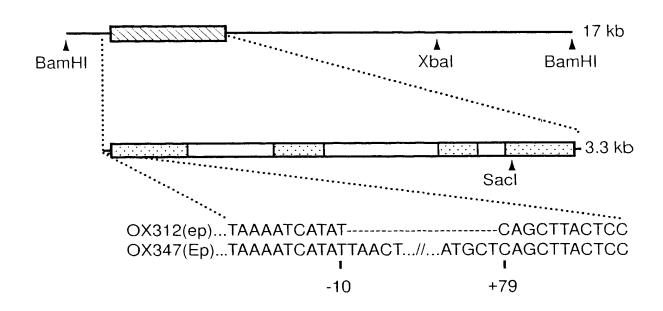


FIGURE 5



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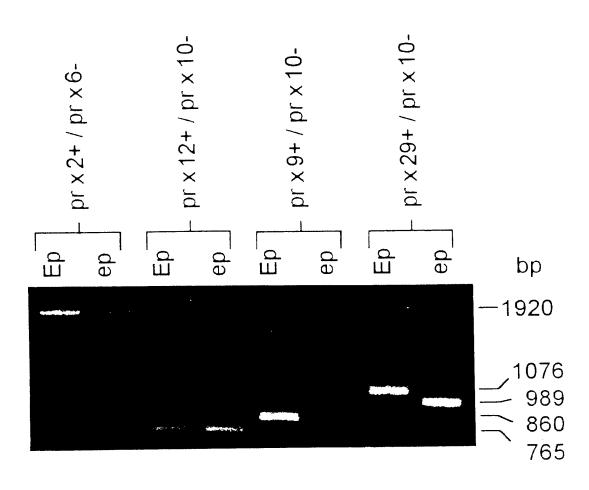


FIGURE 6

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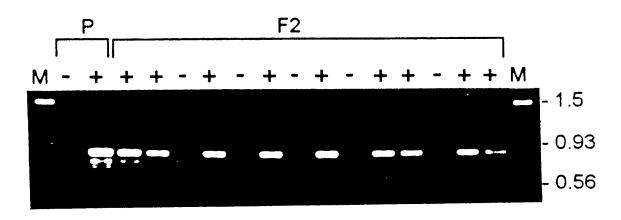


FIGURE 7A

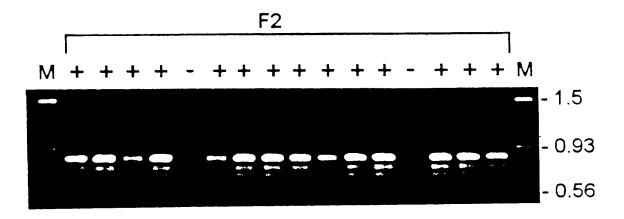
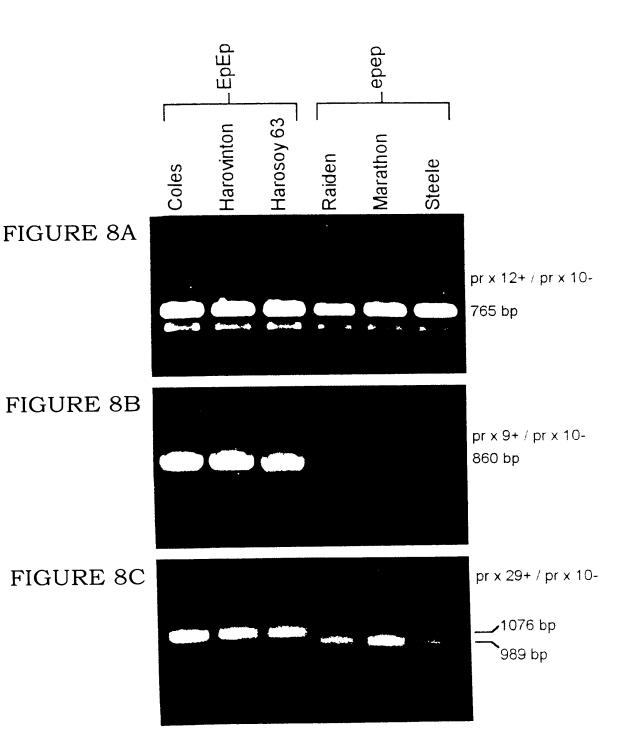


FIGURE 7B

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FIGURE 9B

